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## RAW SEQUENCE LISTING

DATE: 12/17/2001

PATENT APPLICATION: US/09/784,077

TIME: 14:45:34

Input Set : N:\Crf3\RULE60\09784077.txt

Output Set: N:\CRF3\12172001\I784077.raw

## SEQUENCE LISTING

## 4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: NATSUKA, SHUNJI

7 GERSTEN, KEVIN M.

8 LOWE, JOHN B.

10 (ii) TITLE OF INVENTION: MURINE ALPHA (1,3) FUCOSYLTRANSFERASE

11 FUC-TVII, DNA ENCODING THE SAME, METHOD FOR PREPARING THE

12 SAME, ANTIBODIES RECOGNIZING THE SAME, IMMUNOASSAYS FOR

13 DETECTING THE SAME, PLASMIDS CONTAINING SUCH DNA

15 (iii) NUMBER OF SEQUENCES: 4

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &amp; NEUSTADT,

19 P.C.

20 (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

21 (C) CITY: ARLINGTON

22 (D) STATE: VA

23 (E) COUNTRY: USA

24 (F) ZIP: 22202

26 (v) COMPUTER READABLE FORM:

27 (A) MEDIUM TYPE: Floppy disk

28 (B) COMPUTER: IBM PC compatible

29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

32 (vi) CURRENT APPLICATION DATA:

C--&gt; 33 (A) APPLICATION NUMBER: US/09/784,077

C--&gt; 34 (B) FILING DATE: 16-Feb-2001

35 (C) CLASSIFICATION:

37 (vii) PRIOR APPLICATION DATA:

38 (A) APPLICATION NUMBER: US 08/613,098

39 (B) FILING DATE: 08-MAR-1996

44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: LAVALLEYE, JEAN-PAUL

46 (B) REGISTRATION NUMBER: 31,451

47 (C) REFERENCE/DOCKET NUMBER: 2363-114-55

49 (ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 703-413-3000

51 (B) TELEFAX: 703-413-2220

54 (2) INFORMATION FOR SEQ ID NO: 1:

56 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 3594 base pairs

58 (B) TYPE: nucleic acid

59 (C) STRANDEDNESS: double

60 (D) TOPOLOGY: linear

62 (ii) MOLECULE TYPE: cDNA

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

69 ACAACAGGA AGGACAGCAG GCTCTGGCAG CCAGAAGCCT GTGGCCCCAA GCTGGCAGGA

60

71 TGGCCCCCTT CCTGCAGGTC CCCACAGCC TTCTGGGTTT CTGACACGAG AGAAGAGGTG

120

ENTERED

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73	GGGCGGGGTG	AAGTGAATC	TGAAGCCAAA	ATGTGACTCT	CCTGGGGTCA	CCAGCTTGGG	180
75	GAGAGGTGAA	GAAAGATGCC	GGGCGGGA	CAAAGGGGCA	GATATCACTA	TGGTTATCTT	240
77	ACTAAGCACA	GAGTAACTGA	AAAAGCAAGG	GTACCGCTGC	CCACCTCGTG	CCCACCTTAC	300
79	GTTATACCTC	AAACCAGCTA	GATAGTTTCT	GATGGCACCC	ATACCCTCCC	TTCCCCTTTA	360
81	GGCATTGCGC	AAGCTCTCCA	CCACAATCTG	GAAGTTATAC	CCTGCGAGGG	GATGGGCAGG	420
83	GCACTTCTGA	GGTGCCAAATC	AGCCTGCACT	CGCCTCTGCC	CTGGCCATGG	CACCTGCTGTC	480
85	AGTTTCTTGG	TACCTGTCTC	AACAGCAGCC	TTGTACAGTG	AGACTATGGC	TGGCGGTGGG	540
87	GGTGGGGGCA	GGAATCCTAG	AAGCACAGGA	GTGACATAGG	GTCGGGTCGG	GCAGAGCGAA	600
89	GTGTAGGAGG	TGATCCCCAA	AGGGATGCTG	GGGACGATCT	GGCCAACACT	GTCCTCCCAT	660
91	TCAAAACTCC	CAGTCTGGAG	CTCTGGGACA	TGGACAAGCC	AGGCCTGCTA	TTCTCCATAC	720
93	AGGGCTCCAT	AGTGTCTGGC	TCAGCAGAGT	GGGGGATCTG	GTGGGGATGG	AGGAAGCTTA	780
95	GCTAAAAGCT	TTGTATAGGC	TGAAGCTCTG	AGTGACCCTG	CTGGGCCACC	CTACCCTGGT	840
97	CTGGGCTGGG	TCATTGCATC	CCCAGATTGG	AAGGCTTGGT	GAGATGGAGA	GGAACCTTGG	900
99	CTACAAGCTA	TAGCTTTGCC	CACCAGAGCC	TGCTGGAGGG	GAATCAAACA	AGCCTGGACC	960
101	TGAGGCTGGG	ACTAGCTTTC	CTGTTTCTGG	AGTGGATGCC	AACCCCTGTC	CCACCAGCCT	1020
103	GCCTGTCCAC	GCCAGGGACA	CACAGACTCC	TTCCCTTTCC	AGACTGGA	GCCCCCTCCT	1080
105	GGGAGAGCAG	GAAGGAAGCA	ACCTGCAACT	CTTCCAGCCC	TGGACCTTGG	GCTGAACCTA	1140
107	CAGTTCAAGG	TTGTATGCT	CACAGGTCTT	GGCAGGGAAA	GATAAGAATC	CCCAGGGCAC	1200
109	CCTCCCCCCC	GCCCCCAGT	CCACTGCAGG	TAGCTTCTGG	GTCTGCCCTT	CAGGGCAAGT	1260
111	GCTGACGCTC	CATGACATG	TGATGGGGCC	CTTTTCTGAG	GATGACAATT	CTGAGAACAA	1320
113	GGCATTTTTT	TAGAGGTGGC	AGAACAGCAT	TTTGTGATGC	CCGAGGATCT	GGGAGCACAG	1380
115	GTCCAGCTTA	ATGAGGGATT	GGAGGAAGTG	GGTATCATCA	TTACAGGGAG	GGGCCTCTGT	1440
117	GGCTCCTGG	GAAATGCAG	TTGCTCTCTT	TGGGTGGCCT	GGGGTTGTGT	GGTGGGCAGA	1500
119	GGACGGAGGT	GCTCATTTGG	GGAAGGGATC	ACTTCTGCTC	AGAGTGCTCG	CAAGGGCCTT	1560
121	TCCTTTTCCT	GAAGGCAAGC	AGGCCTCCTC	CTCCTCCTCT	TCCTCCTTCT	CCTCTTCCTC	1620
123	CTCTTTCTCC	ATATGCCTAG	CTGGTCATTT	CTAGGGACCA	GCATGGTTGG	GAAGGGGGCC	1680
125	TTGTCTTGGC	CTTCTCTTG	TCTCAATTCC	CTCTTTGAGC	AGAAGACGGG	GTGGGTGGGG	1740
127	TAGGATTGGA	TAGTGGTTGA	TGCCAAAGAT	TGAAGGGGTA	GGGCGGGGCA	GAAGTGGGAA	1800
129	GGTCCTGGC	TTCTCACCCT	TGGTAGATGG	TGAGGAGCCC	CAGAGGTTGA	GCTGAGCAGC	1860
131	AGCTGTGATT	TCAGGGTGCC	TCTGTTGGAG	AGGCTGCTGT	GATTTGAAAA	TCTTCTTTCC	1920
133	TTGGTGACAA	TTCCAGAAGG	CTCCAGATGA	ATTGTATTGG	TGAGTGCCCTG	GCCCTTAAGC	1980
135	AGTCCCAGCT	GGGGATGATG	GGGATTTATG	GGTGTCCCTG	AGCCTAGGGT	GACAGGGCCT	2040
137	CTCCTTTTTT	TTTTATTCTG	CTTCAGGGTA	CCACCCACCC	AGGAGGCTGC	GGGCCTGGGG	2100
139	CGGCCTAGCT	GGAGGAGCAA	CATTATGGT	AATTTGGTTT	TTCTGGCTGT	GGGGATCAGC	2160
141	TCCTGGAAGT	GCCCCGTGTC	CTCAGTCCAC	ACTCACCATC	CTTATCTGGC	ACTGGCCTTT	2220
143	CACCAACCGG	CCGCCAGAGC	TACCTGGTGA	CACCTGCATC	CGCTATGGCA	TGGCCAGCTG	2280
145	CCGTCTGAGT	GCTAACCAGG	GCCTGTAGC	CAGTGCTGAT	GCTGTGGTCT	TCCACCACCG	2340
147	TGAGCTGCAA	ACCCGGCAAT	CTCTCCTACC	CCTGGACCAG	AGGCCACACG	GACAGCCTTG	2400
149	GGTCTGGGCC	TCCATGGAAT	CGCCAGTAA	TACCCATGGT	CTCCATCGCT	TCCGGGGCAT	2460
151	CTTCAACTGG	GTGCTGAGCT	ATCGGCGTGA	TTCAGATATC	TTTGTACCCT	ACGGTCGCTT	2520
153	GGAGCCTCTC	TCTGGGCCCA	CATCCCCACT	ACCGGCCAAA	AGCAGGATGG	CTGCCTGGGT	2580
155	GATCAGCAAT	TTCCAGGAGC	GGCAGCAGCG	TGCAAAGCTG	TACCGGCAGC	TGGCCCCCTCA	2640
157	TCTGCAGGTG	GATGTGTTCTG	GTCGCGCCAG	CGGACGGCCC	CTATGCGCTA	ATTGTCTGCT	2700
159	GCCCACCTTG	GCCCCGTACC	GCTTCTACCT	GGCCTTTGAG	AACTCACAGC	ATCGGGACTA	2760
161	CATCACTGAG	AAGTTCTGGC	GCAATGCCCT	GGCGGCTGGT	GCTGTACCCG	TGGCGCTGGG	2820
163	ACCTCCTCGG	GCCACCTACG	AGGCTTTTGT	GCCACCAGAT	GCCTTTGTAC	ACGTGGACGA	2880
165	CTTCAGCTCT	GCCCCGTGAAC	TGGCTGTCTT	CCTCGTCAGC	ATGAATGAGA	GTCGTTATCG	2940
167	TGGCTTCTTT	GCTTGGCGAG	ACCGGCTCCG	TGTGCGGCTC	CTGGGTGACT	GGAGGGAGCG	3000
169	CTTCTGCACC	ATCTGTGCCC	GCTACCCTTA	CTTGCCCCGC	AGCCAGGTCT	ATGAAGACCT	3060

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```

171 TGAAAGCTGG TTCCAGGCTT GAACTCCTGC TGCTGGGAGA GGCTGGATGG GTGGGAGACT 3120
173 GATGTTGAAA CCAAAGAGCT GGGCATCCAG GCTTTTGGTC ACCATGGCAC TACCCCAAGG 3180
175 CTTTTCTGT TCAGTGAGCA GGAATTCAGG ATATAAGGAG AAGACTGGGC TGAGATACCC 3240
177 TGGTGGGCTT TAGAGTAGGG GCCCAGGATA AGAGACAATG AATTAATGAG GAGCATATGG 3300
179 GGAAGGTGGC TGAGGTGCC TGAATTACCT TGACCCATGG CTGAAGGCTC CATGCCCATG 3360
181 GCTGGAGCTG GGACCCTACA CTTCTATAGT CAAGGTGCTT AGCCTCAAGG TTGCAGATGC 3420
183 ACCCTCTAGT ACTCTGGGTG CAGACTGTAC ACTGGGCGCA GGGGGTTGTG GAAGGACAGT 3480
185 GCAGATGATT CTGGGCTTTT GACACCACAG TTCCCCCAGG GAAAGAGGCA CTACTAATAA 3540
187 AAACACTGAC AGAAATCTCC TGGTCAAGTC TGTTAGGCAG CAGAGCTCGA ATTC 3594

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189 (2) INFORMATION FOR SEQ ID NO: 2:

191 (i) SEQUENCE CHARACTERISTICS:

192 (A) LENGTH: 393 amino acids

193 (B) TYPE: amino acid

194 (C) STRANDEDNESS: single

195 (D) TOPOLOGY: linear

197 (ii) MOLECULE TYPE: protein

202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

204 Met Pro Thr Pro Cys Pro Pro Ala Cys Leu Ser Thr Pro Gly Thr His
205 1 5 10 15
207 Arg Leu Leu Pro Phe Pro Asp Trp Lys Ala Pro Ser Trp Glu Ser Arg
208 20 25 30
210 Lys Glu Ala Thr Cys Asn Ser Ser Ser Pro Gly Pro Trp Ala Glu Pro
211 35 40 45
213 Thr Val Gln Met Asn Cys Ile Gly Tyr His Pro Thr Arg Arg Leu Arg
214 50 55 60
216 Ala Trp Gly Gly Leu Ala Gly Gly Ala Thr Phe Met Val Ile Trp Phe
217 65 70 75 80
219 Phe Trp Leu Trp Gly Ser Ala Pro Gly Ser Ala Pro Val Pro Gln Ser
220 85 90 95
222 Thr Leu Thr Ile Leu Ile Trp His Trp Pro Phe Thr Asn Arg Pro Pro
223 100 105 110
225 Glu Leu Pro Gly Asp Thr Cys Thr Arg Tyr Gly Met Ala Ser Cys Arg
226 115 120 125
228 Leu Ser Ala Asn Arg Ser Leu Ala Ser Ala Asp Ala Val Val Phe
229 130 135 140
231 His His Arg Glu Leu Gln Thr Arg Gln Ser Leu Leu Pro Leu Asp Gln
232 145 150 155 160
234 Arg Pro His Gly Gln Pro Trp Val Trp Ala Ser Met Glu Ser Pro Ser
235 165 170 175
237 Asn Thr His Gly Leu His Arg Phe Arg Gly Ile Phe Asn Trp Val Leu
238 180 185 190
240 Ser Tyr Arg Arg Asp Ser Asp Ile Phe Val Pro Tyr Gly Arg Leu Glu
241 195 200 205
243 Pro Leu Ser Gly Pro Thr Ser Pro Leu Pro Ala Lys Ser Arg Met Ala
244 210 215 220
246 Ala Trp Val Ile Ser Asn Phe Gln Glu Arg Gln Gln Arg Ala Lys Leu
247 225 230 235 240
249 Tyr Arg Gln Leu Ala Pro His Leu Gln Val Asp Val Phe Gly Arg Ala
250 245 250 255

```

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```

252   Ser Gly Arg Pro Leu Cys Ala Asn Cys Leu Leu Pro Thr Leu Ala Arg
253           260           265           270
255   Tyr Arg Phe Tyr Leu Ala Phe Glu Asn Ser Gln His Arg Asp Tyr Ile
256           275           280           285
258   Thr Glu Lys Phe Trp Arg Asn Ala Leu Ala Ala Gly Ala Val Pro Val
259           290           295           300
261   Ala Leu Gly Pro Pro Arg Ala Thr Tyr Glu Ala Phe Val Pro Pro Asp
262           305           310           315           320
264   Ala Phe Val His Val Asp Asp Phe Ser Ser Ala Arg Glu Leu Ala Val
265           325           330           335
267   Phe Leu Val Ser Met Asn Glu Ser Arg Tyr Arg Gly Phe Phe Ala Trp
268           340           345           350
270   Arg Asp Arg Leu Arg Val Arg Leu Leu Gly Asp Trp Arg Glu Arg Phe
271           355           360           365
273   Cys Thr Ile Cys Ala Arg Tyr Pro Tyr Leu Pro Arg Ser Gln Val Tyr
274           370           375           380
276   Glu Asp Leu Glu Ser Trp Phe Gln Ala
277           385           390

```

279 (2) INFORMATION FOR SEQ ID NO: 3:

281 (i) SEQUENCE CHARACTERISTICS:

282 (A) LENGTH: 41 base pairs

283 (B) TYPE: nucleic acid

284 (C) STRANDEDNESS: single

285 (D) TOPOLOGY: linear

287 (ii) MOLECULE TYPE: other nucleic acid

288 (A) DESCRIPTION: /desc = "SYNTHETIC PRIMER"

293 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

295 GCGCGGATCC CACCATCCTT ATCTGGCACT GGCCTTTCAC C

41

297 (2) INFORMATION FOR SEQ ID NO: 4:

299 (i) SEQUENCE CHARACTERISTICS:

300 (A) LENGTH: 44 base pairs

301 (B) TYPE: nucleic acid

302 (C) STRANDEDNESS: single

303 (D) TOPOLOGY: linear

305 (ii) MOLECULE TYPE: other nucleic acid

306 (A) DESCRIPTION: /desc = "SYNTHETIC PRIMER"

311 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

313 GCGCGGATCC AGTTCAAGCC TGGAACCAGC TTTCAAGGTC CTTC

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/784,077

DATE: 12/17/2001

TIME: 14:45:35

Input Set : N:\Crf3\RULE60\09784077.txt

Output Set: N:\CRF3\12172001\I784077.raw

L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]